



SEQUENCE LISTING

COPY OF PAPERS
ORIGINALLY FILED

<110> Wang, Jian
Xi, Lei
Prosen, Dennis E.
MJ Bioworks, Inc.

<120> Improved Nucleic Acid Modifying Enzymes

<130> 020130-000111US

<140> US 09/870,353

<141> 2001-05-30

<150> US 60/207,567

<151> 2000-05-26

<150> US 09/640,958

<151> 2000-08-16

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 189

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
sequence non-specific double-stranded nucleic acid
binding protein Ssod7d

<220>

<221> CDS

<222> (1)..(189)

<223> Ssod7d

<400> 1

gcaaccgtaa agttcaagta caaaggcgaa gaaaaagagg tagacatctc caagatcaag 60
aaagtatggc gtgtgggcaa gatgatctcc ttcacctacg acgagggcgg tggcaagacc 120
ggccgtggtg cggtaagcga aaaggacgcg ccgaaggagc tgctgcagat gctggagaag 180
cagaaaaag 189

<210> 2

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
sequence non-specific double-stranded nucleic acid
binding protein Ssod7d

<400> 2

Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile
1 5 10 15
Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
20 25 30

Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys
35 40 45
Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
50 55 60

<210> 3
<211> 1899
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
Ssod7d-deltaTaq

<220>
<221> CDS
<222> (1)..(1899)
<223> Ssod7d-deltaTaq

<400> 3
atgattacga attcgagcgc aaccgtaaag ttcaagtaca aaggcgaaga aaaagaggta 60
gacatctcca agatcaagaa agtatggcgt gtgggcaaga tgatctcctt cacctacgac 120
gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
ctgcagatgc tggagaagca gaaaaagggc ggcggtgtca ctagtcccaa ggccctggag 240
gagggccccct ggcccccgcc ggaagggggc ttctgtgggt ttgtgctttc ccgcaaggag 300
cccatgtggg ccgatcttct ggccctggcc gccgccaggg ggggcccggg ccaccgggcc 360
cccagacctt ataaagccct cagggacctg aaggaggcgc gggggcttct cgccaaagac 420
ctgagcgttc tggccctgag ggaaggcctt ggccctccgc ccggcgacga ccccatgctc 480
ctcgctacc tcttgaccc ttccaacacc acccccagg ggggtggccc gcgctacggc 540
ggggagtggg cggaggaggc gggggagcgg gccgcccttt ccgagaggct cttcgccaac 600
ctgtggggga ggcttgaggg ggaggagagg ctcccttggc tttaccggga ggtggagagg 660
cccctttccg ctgtcctggc ccacatggag gccacggggg tgcgcctgga cgtggcctat 720
ctcagggcct tgtccctgga ggtggccgag gagatcgccc gcctcgaggc cgaggtcttc 780
cgcttgccg gccacccctt caacctcaac tcccgggacc agctggaaag ggtcctcttt 840
gacgagctag ggcttcccgc catcggaag acggagaaga ccggcaagcg ctccaccagc 900
gccgcgctcc tggaggccct ccgcgaggcc caccctatcg tggagaagat cctgcagtac 960
cgggagctca ccaagctgaa gagcacctac attgaccctt tgccggacct catccacccc 1020
aggacggggc gcctccacac ccgcttcaac cagacggcca cggccacggg caggctaagt 1080
agctccgata ccaacctcca gaacatcccc gtccgcaccc cgcttgggca gaggatccgc 1140
cgggccttca tcgccgagga ggggtggcta ttgggtggcc tggactatag ccagatagag 1200
ctcagggtgc tggccacact ctccggcgac gagaacctga tccgggtctt ccaggagggg 1260
cgggacatcc acacggagac cgccagctgg atgttcggcg tcccccgga ggccgtggac 1320
cccctgatgc gccgggccc caagaccatc aacttcgggg tctctacgg catgtcggcc 1380
caccgcctct cccaggagct agccatccct tacgaggagg cccaggcctt cattgagcgc 1440
tactttcaga gcttcccaa ggtgcggggc tggattgaga agaccctgga ggagggcagg 1500
aggcgggggt acgtggagac cctcttcggc cgccgcgct acgtgccaga cctagaggcc 1560
cgggtgaaga gcgtgcggga ggccggccgag cgcattggcct tcaacatgcc cgtccagggc 1620
accgcgccc acctcatgaa gctggctatg gtgaagctct tcccaggct ggaggaaatg 1680
ggggccagga tgcctcttca ggtccacgac gagctggctc tcgaggcccc aaaagagagg 1740
gcggaggccg tggcccggct ggccaaggag gtcattggagg ggggtgatcc cctggccgtg 1800
ccctggagg tggaggtggg gataggggag gactggctct ccgccaagga gggcattgat 1860
ggccgcggcg gaggcgggca tcatcatcat catcattaa 1899

<210> 4
<211> 632
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
Ssod7d-deltaTaq

<400> 4

```
Met Ile Thr Asn Ser Ser Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu
 1           5           10           15
Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly
          20           25           30
Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg
          35           40           45
Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
          50           55           60
Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala Leu Glu
          65           70           75           80
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
          85           90           95
Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala
          100          105          110
Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
          115          120          125
Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu
          130          135          140
Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu
          145          150          155          160
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
          165          170          175
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala
          180          185          190
Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu
          195          200          205
Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala
          210          215          220
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
          225          230          235          240
Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Ile Ala Arg Leu Glu
          245          250          255
Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
          260          265          270
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile
          275          280          285
Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
          290          295          300
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
          305          310          315          320
Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp
          325          330          335
Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
          340          345          350
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
          355          360          365
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile
          370          375          380
Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
          385          390          395          400
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
          405          410          415
Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe
          420          425          430
Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
          435          440          445
```

Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
 450 455 460
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg
 465 470 475 480
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
 485 490 495
 Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
 500 505 510
 Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala
 515 520 525
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
 530 535 540
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met
 545 550 555 560
 Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
 565 570 575
 Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met
 580 585 590
 Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile
 595 600 605
 Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg Gly Gly
 610 615 620
 Gly Gly His His His His His His
 625 630

<210> 5
 <211> 2763
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Ssod7d/full-length Taq

<220>
 <221> CDS
 <222> (1)..(2763)
 <223> Ssod7d/full-length Taq

<400> 5
 atgattacga attcgagcgc aaccgtaaaag ttcaagtaca aaggcgaaga aaaagaggta 60
 gacatctcca agatcaagaa agtatggcgt gtgggcaaga tgatctcctt cacctacgac 120
 gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
 ctgcagatgc tggagaagca gaaaaagggc ggcggtgtca ctagtgggat gctgcccttc 240
 tttgagccca agggcgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 300
 cagccctga agggcctcac caccagccgg ggggagccgg tgcaggcggg ctacggcttc 360
 gccaaagacc tcctcaaggc cctcaaggag gacggggacg cggatgacgt ggtctttgac 420
 gccaaaggccc cctccttcgg ccacgaggcc tacggggggg acaaggcggg ccgggcccccc 480
 acgccagagg actttccccg gcaactcgcc ctcatcaagg agctggtgga cctcctgggg 540
 ctggcgcgcc tcgaggtccc gggctacgag gcgagcgacg tcctggccag cctggccaag 600
 aaggcggaaa aggaggggcta cgaggtccgc atcctcaccg ccgacaaaga cctttaccag 660
 ctcccttcgg accgcatcca cgctcctccac cccgaggggt acctcatcac cccggcctgg 720
 ctttgggaaa agtacggcct gaggccccgac cagtggggcg actaccgggc cctgaccggg 780
 gacgagtcgg acaaccttcc cggggtcaag ggcacggggg agaagacggc gaggaagctt 840
 ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccggc 900
 atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 960
 gtgcgcaccg acctgccccct ggaggtggac ttcgccaataa ggcggggagc cgaccgggag 1020
 aggcttaggg cctttctgga gaggtctgag tttggcagcc tcctccacga gttcggcctt 1080
 ctggaaagcc ccaaggccct ggaggaggcc ccctggcccc cgccggaagg ggccttcgtg 1140
 ggctttgtgc tttcccgcga ggagcccatg tgggcccgat ttctggccct ggccgcccgc 1200

```

aggggggggccc ggggtccaccg ggccccccgag ccttataaag ccctcagggga cctgaaggag 1260
gcgcggggggc ttctcgccaa agacctgagc gttctggccc tgaggggaagg ccttggcctc 1320
ccgcccggcg acgaccccat gctcctcgcc tacctcctgg acccttccaa caccaccccc 1380
gaggggggtgg cccggcgcta cggcggggag tggacggagg aggcggggga gcggggccgccc 1440
ctttccgaga ggctcttcgc caacctgttg gggaggcttg agggggagga gaggctcctt 1500
tggctttacc gggaggtgga gaggccccctt tccgctgtcc tggccacat ggaggccacg 1560
ggggtgcccc tggacgtggc ctatctcagg gccttggtccc tggaggtggc cgaggagatc 1620
ggccgcctcg aggcgaggt cttccgcctg gccggccacc ccttcaacct caactccccg 1680
gaccagctgg aaagggtcct ctttgacgag ctagggtctc ccgccatcg caagacggag 1740
aagaccggca agcgtccac cagcgccgcc gtcttgagg ccctccgca gggccacccc 1800
atcgtggaga agatcctgca gtaccgggag ctaccaagc tgaagagcac ctacattgac 1860
cccttgccgg acctcatcca ccccaggagc ggccgcctcc acaccgctt caaccagacg 1920
gccacggcca cgggcaggct aagtagctcc gatcccaacc tccagaacat ccccgctccg 1980
accccgcttg ggcagaggat ccgcccggcc ttcatcgccg aggaggggtg gctattggtg 2040
gccctggact atagccagat agagctcagg gtgctggccc acctctccgg cgacgagaac 2100
ctgatccggg tcttccagga gggcggggac atccacacgg agaccgccag ctggatgttc 2160
ggcgctcccc gggaggccgt ggacccccctg atgcgccggg cggccaagac catcaacttc 2220
ggggctcctc acggcatgtc ggcccaccgc ctctcccagg agctagccat cccttacgag 2280
gaggcccagg ccttcattga gcgctacttt cagagcttcc ccaaggtgcg ggccctggatt 2340
gagaagacct tggaggaggg caggaggcgg gggtagctgg agacctctt cggccgccgc 2400
cgctacgtgc cagacctaga ggcccgggtg aagagcgtgc gggaggcggc cgagcgcag 2460
gccttcaaca tgcccgcca gggcaccgcc gccgacctca tgaagctggc tatggtgaag 2520
ctcttcccc ggttgaggga aatggggggc aggatgtctc ttcaggtcca cgacgagctg 2580
gtcctcgagg ccccaaaaga gagggcggag gccgtggccc ggctggccaa ggaggtcatg 2640
gagggggtgt atccccggc cgtgccccctg gaggtggagg tggggatagg ggaggactgg 2700
ctctccgcca aggagggcat tgatggccgc ggcggaggcg ggcacatca tcatcatcat 2760
taa

```

<210> 6
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Ssod7d/full-length Taq

```

<400> 6
Met Ile Thr Asn Ser Ser Ala Thr Val Lys Phe Lys Tyr Lys Gly Glu
 1             5             10             15
Glu Lys Glu Val Asp Ile Ser Lys Ile Lys Lys Val Trp Arg Val Gly
             20             25             30
Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg
             35             40             45
Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
             50             55             60
Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Gly Met Leu Pro Leu
             65             70             75             80
Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly His His Leu Ala
             85             90             95
Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr Ser Arg Gly Glu
             100            105            110
Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu Leu Lys Ala Leu
             115            120            125
Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp Ala Lys Ala Pro
             130            135            140
Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala Gly Arg Ala Pro
             145            150            155            160
Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile Lys Glu Leu Val
             165            170            175

```

Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	180	185	190
Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	195	200	205
Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	210	215	220
Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	225	230	235
Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	245	250	255
Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	260	265	270
Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	275	280	285
Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	290	295	300
Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	305	310	315
Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	325	330	335
Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	340	345	350
Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu		355	360	365
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	370	375	380
Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	385	390	395
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	405	410	415
Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	420	425	430
Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	435	440	445
Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	450	455	460
Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	465	470	475
Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	485	490	495
Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	500	505	510
Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	515	520	525
Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	530	535	540
Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	545	550	555
Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	565	570	575
Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	580	585	590
Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	595	600	605
Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	610	615	620
Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	625	630	635
Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	645	650	655

Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile		
			660					665					670				
Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu		
		675					680					685					
Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val		
		690				695					700						
Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe		
705					710					715					720		
Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys		
				725					730					735			
Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser		
			740					745					750				
Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg		
		755					760					765					
Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu		
	770					775					780						
Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg		
785					790					795					800		
Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala		
				805					810					815			
Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp		
			820					825					830				
Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met		
		835					840					845					
Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Val	Leu	Glu	Ala		
	850					855					860						
Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu	Val	Met		
865					870					875					880		
Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Ile		
				885					890					895			
Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	Gly	Ile	Asp	Gly	Arg	Gly	Gly		
			900					905					910				
Gly	Gly	His	His	His	His	His	His										
		915					920										

<210> 7
 <211> 2535
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Pfu-Ssod7d

<220>
 <221> CDS
 <222> (1) .. (2535)
 <223> Pfu-Ssod7d

<400> 7
 atgatttttag atgtggatta cataactgaa gaaggaaaac ctgttatttag gctatttcaaa 60
 aaagagaacg gaaaatttaa gatagagcat gatagaactt ttagaccata catttacgct 120
 cttctcaggg atgattcaaa gattgaagaa gttaagaaaa taacggggga aaggcatgga 180
 aagattgtga gaattgttga tgtagagaag gttgagaaaa agtttctcgg caagcctatt 240
 accgtgtgga aactttatatt ggaacatccc caagatgttc ccactatttag agaaaaagtt 300
 agagaacatc cagcagttgt ggacatcttc gaatacgata ttccatttgc aaagagatac 360
 ctcatcgaca aagcctaata accaatggag ggggaagaag agctaaagat tcttgccctc 420
 gatatagaaa cctctatca cgaaggagaa gagtttgga aaggcccaat tataatgatt 480
 agttatgcag atgaaaatga agcaaaggtg attacttgga aaaacataga tcttccatac 540
 gttgaggttg tatcaagcga gagagagatg ataaagagat ttctcaggat tatcaggggag 600

```

aaggatcctg acattatagt tacttataat ggagactcat tcgacttccc atatttagcg 660
aaaagggcag aaaaacttgg gattaaatta accattggaa gagatggaag cgagcccaag 720
atgcagagaa taggcgatat gacggctgta gaagtcaagg gaagaatata tttcgacttg 780
tatcatgtaa taacaaggac aataaatctc ccaacatata cactagaggc tgtatatgaa 840
gcaatttttg gaaagccaaa ggagaaggta tacgccgacg agatagcaaa agcctgggaa 900
agtggagaga accttgagag agttgccaaa tactcgatgg aagatgcaaa ggcaacttat 960
gaactcggga aagaattcct tccaatggaa attcagcttt caagattagt tggacaacct 1020
ttatgggatg tttcaaggtc aagcacaggg aaccttgtag agtggttctt acttaggaaa 1080
gcctacgaaa gaaacgaagt agctccaaac aagccaagtg aagaggagta tcaaagaagg 1140
ctcagggaga gctacacagg tggattcggt aaagagccag aaaaggggtt gtgggaaaac 1200
atagtatacc tagatttttag agccctatat ccctcgatta taattacca caatgtttct 1260
cccgatactc taaatcttga gggatgcaag aactatgata tcgctcctca agtagggcac 1320
aagttctgca aggacatccc tggttttata ccaagtctct tgggacattt gttagaggaa 1380
agacaaaaga ttaagacaaa aatgaaggaa actcaagatc ctatagaaaa aatactcctt 1440
gactatagac aaaaagcgat aaaactctta gcaaattctt tctacggata ttatggctat 1500
gcaaaagcaa gatggtactg taaggagtgt gctgagagcg ttactgcctg gggaagaaag 1560
tacatcgagt tagtatggaa ggagctcgaa gaaaagtttg gatttaaagt cctctacatt 1620
gacactgatg gtctctatgc aactatccca ggaggagaaa gtgaggaaat aaagaaaaag 1680
gctctagaat ttgtaaaata cataaattca aagctccctg gactgctaga gcttgaatat 1740
gaagggtttt ataagagggg attcttcggt acgaagaaga ggtatgcagt aatagatgaa 1800
gaagggaaaag tcattactcg tggtttagag atagttagga gagattggag tgaaattgca 1860
aaagaaactc aagctagagt tttggagaca atactaaaac acggagatgt tgaagaagct 1920
gtgagaatag taaaagaagt aatacaaaaag cttgccatt atgaaattcc accagagaag 1980
ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
gtagctgttg caaagaaact agctgctaaa ggagttaaaa taaagccagg aatggtaatt 2100
ggatcacatg tacttagagg cgatgggtcca attagcaata gggcaattct agctgaggaa 2160
tacgatccca aaaagcacaa gtatgacgca gaatattaca ttgagaacca ggttcttcca 2220
gcggtactta ggatattgga gggatttgga tacagaaaag aagacctcag ataccaaaaag 2280
acaagacaag tcggcctaac ttcttggtt aacattaaaa aatccggtac cggcgggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cgggtggcaag 2460
accggccgtg gtgcggtaag cgaaaaggac gcgccgaagg agctgctgca gatgctggag 2520
aagcagaaaa agtga                                     2535

```

<210> 8
 <211> 844
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Pfu-Ssod7d

```

<400> 8
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
  1             5             10            15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
          20             25             30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
          35             40             45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
          50             55             60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
          65             70             75             80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
          85             90             95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
          100            105            110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
          115            120            125

```


Met	Glu	Gly	Glu	Glu	Glu	Leu	Lys	Ile	Leu	Ala	Phe	Asp	Ile	Glu	Thr	130	135	140
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Gly	Lys	Gly	Pro	Ile	Ile	Met	Ile	145	150	155
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile	165	170	175
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys	180	185	190
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr	195	200	205
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu	210	215	220
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	225	230	235
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	245	250	255
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr	260	265	270
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu	275	280	285
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Ser	Gly	Glu	Asn	290	295	300
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr	305	310	315
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu	325	330	335
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	340	345	350
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala	355	360	365
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser	370	375	380
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn	385	390	395
Ile	Val	Tyr	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	405	410	415
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Leu	Glu	Gly	Cys	Lys	Asn	Tyr	420	425	430
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly	435	440	445
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile	450	455	460
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu	465	470	475
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	485	490	495
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	500	505	510
Ser	Val	Thr	Ala	Trp	Gly	Arg	Lys	Tyr	Ile	Glu	Leu	Val	Trp	Lys	Glu	515	520	525
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly	530	535	540
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Ser	Glu	Glu	Ile	Lys	Lys	Lys	545	550	555
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu	565	570	575
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	580	585	590
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly	595	600	605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 610 615 620
 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 625 630 635 640
 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 645 650 655
 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 660 665 670
 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 675 680 685
 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 690 695 700
 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 705 710 715 720
 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 725 730 735
 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 740 745 750
 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 755 760 765
 Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Ala Thr Val
 770 775 780
 Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
 785 790 795 800
 Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
 805 810 815
 Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
 820 825 830
 Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
 835 840

<210> 9
 <211> 1904
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Sac7d-deltaTaq

<220>
 <221> CDS
 <222> (1)..(1904)
 <223> Sac7d-deltaTaq

<400> 9
 atgattacga attcgacggt gaaggtaaag ttcaagtata aggggtgaaga gaaagaagta 60
 gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tgggtgtcctt tacctatgac 120
 gacaatggta agacaggttag aggagctgta agcgagaaag atgctccaaa agaattatta 180
 gacatggttag caagagcaga aagagagaag aaaggcgggc gtgtcactag tcccaaggcc 240
 ctggaggagg ccccttgccc cccgccggaa ggggccttcg tgggctttgt gctttcccgc 300
 aaggagccca tgtgggcccga tcttctggcc ctggccgccg ccaggggggg ccgggtccac 360
 cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 420
 aaagacctga gcgttctggc cctgaggga ggccttgccc tcccgcccgg cgacgacccc 480
 atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgagggggg ggcccggcgc 540
 tacggcgggg agtggacgga ggaggcgggg gagcggggcc ccttttccga gaggctcttc 600
 gccaacctgt gggggagggt tgagggggag gagaggctcc ttgggcttta ccgggagggtg 660
 gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 720
 gcctatctca gggccttgct cctggagggt gccgaggaga tcgcccgcct cgaggccggg 780
 tcttccgcct ggccggccac cccttcaacc tcaactcccg ggaccagctg gaaagggtcc 840

```

tctttgacga gctagggctt cccgccatcg gcaagacgga gaagaccggc aagcgctcca 900
ccagcgccgc cgtcctggag gccctccgcg agggccaccc catcgtggag aagatcctgc 960
agtaccggga gctcaccaag ctgaagagca cctacattga ccccttgccg gacctcatcc 1020
accccaggac gggccgcctc cacaccgct tcaaccagac ggccacggcc acgggcaggc 1080
taagtagctc cgatcccaac ctccagaaca tccccgctcg caccgcgtt gggcagagga 1140
tccgcccggc cttcatcgcc gaggaggggt ggctattggt ggccctggac tatagccaga 1200
tagagctcag ggtgctggcc cacctctccg gcgacgagaa cctgatccgg gtcttccagg 1260
aggggcggga catccacacg gagaccgcca gctggatgtt cggcgtcccc cgggaggccg 1320
tggacccccct gatgcgcccg gcggccaaga ccatcaactt cggggtcctc tacggcatgt 1380
cggccaccgc cctctcccag gagctagcca tcccttacga ggaggcccag gccttcattg 1440
agcgctactt tcagagcttc cccaagggtgc gggcctggat tgagaagacc ctggaggagg 1500
gcaggaggcg ggggtacgtg gagaccctct tcggccgccg ccgctacgtg ccagacctag 1560
agggccgggt gaagagcgtg cgggaggcgg ccgagcgcag ggccctcaac atgcccgtcc 1620
agggcaccgc cgccgacctc atgaagctgg ctatggtgaa gctcttcccc aggctggagg 1680
aaatgggggc caggatgctc cttcagggtcc acgacgagct ggtcctcgag gcccctaaaag 1740
agagggcgga ggccgtggcc cggctggcca aggaggtcat ggaggggggt tatcccctgg 1800
ccgtgcccct ggaggtggag gtggggatag gggaggactg gctctccgcc aaggagggga 1860
ttgatggccg cggcggaggc gggcatcatc atcatcatca ttaa 1904

```

<210> 10

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
Sac7d-de_ltaTaq

<400> 10

```

Met Ile Thr Asn Ser Thr Val Lys Val Lys Phe Lys Tyr Lys Gly Glu
  1           5           10           15
Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
          20           25           30
Lys Met Val Ser Phe Thr Tyr Asp Asp Asn Gly Lys Thr Gly Arg Gly
          35           40           45
Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
          50           55           60
Arg Ala Glu Arg Glu Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala
          65           70           75           80
Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
          85           90           95
Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
          100          105          110
Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
          115          120          125
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
          130          135          140
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
          145          150          155          160
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
          165          170          175
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
          180          185          190
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
          195          200          205
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
          210          215          220
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
          225          230          235          240

```

Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
 245 250 255
 Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 260 265 270
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
 275 280 285
 Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 290 295 300
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 305 310 315 320
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
 325 330 335
 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 340 345 350
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 355 360 365
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 370 375 380
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
 385 390 395 400
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 405 410 415
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
 420 425 430
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 435 440 445
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 450 455 460
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
 465 470 475 480
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 485 490 495
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
 500 505 510
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
 515 520 525
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 530 535 540
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
 545 550 555 560
 Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu
 565 570 575
 Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
 580 585 590
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
 595 600 605
 Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg
 610 615 620
 Gly Gly Gly Gly His His His His His His
 625 630

<210> 11

<211> 1965

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
 PL-deltaTaq

<220>
 <221> CDS
 <222> (1)..(1965)
 <223> PL-deltaTaq

<400> 11
 atgattacga attcgaagaa aaagaaaaag aaaaagcgta agaaacgcaa aaagaaaaag 60
 aaaggcggcg gtgtcactag tggcgcaacc gtaaagtcca agtacaaagg cgaagaaaaa 120
 gaggtagaca tctccaagat caagaaagta tggcgtgtgg gcaagatgat ctccttcacc 180
 tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgcgccgaag 240
 gagctgctgc agatgctgga gaagcagaaa aaggcgggcg gtgtcaccag tcccaaggcc 300
 ctggaggagg ccccttgccc cccgccggaa ggggccttcg tgggctttgt gctttcccgc 360
 aaggagccca tgtgggcccga tcttctggcc ctggccgccc ccaggggggg ccgggtccac 420
 cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 480
 aaagacctga gcgttctggc cctgagggaa ggccttgccc tcccgcccgg cgacgacccc 540
 atgctcctcg cctacctcct ggaccttcc aacaccacce ccgagggggg ggcccggcgc 600
 tacggcgggg agtggaacga ggaggcgggg gagcggggcg ccctttccga gaggtctctc 660
 gccaacctgt gggggagggt tgagggggag gagaggctcc tttggcttta cggggagggt 720
 gagaggcccc ttccgctgt cctggccccc atggaggcca cgggggtgcg cctggacgtg 780
 gcctatctca gggccttgct cctggagggt gccgaggaga tcgcccgcct cgaggccgag 840
 gtcttcgcgc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
 ctctttgacg agctagggtt tcccgccatc ggcaagacgg agaagaccgg caagcgtcc 960
 accagcgccg ccgtcctgga ggccctccgc gaggcccacc ccacgtgga gaagatcctg 1020
 cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc 1080
 caccacagga cgggcgcgct ccacaccgc ttcaaccaga cggccacggc cacgggcagg 1140
 ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg 1200
 atccgcccgg ccttcacgct cgaggagggg tggctattgg tggccctgga ctatagccag 1260
 atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag 1320
 gaggggcccgg acatccacac ggagaccgcc agctggatgt tcggcgctcc ccgggaggcc 1380
 gtggaccccc tgatgcgcgg ggcggccaag accatcaact tcggggctct ctacggcatg 1440
 tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
 gagcgctact ttcagagctt cccaagggtg cgggcctgga ttgagaagac cctggaggag 1560
 ggcaggaggc ggggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagacct 1620
 gagggcccgg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc 1680
 cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag 1740
 gaaatggggg ccaggatgct ccttcaggct caccagcagc tggctctcga ggccccaaaa 1800
 gagaggcgcg agggcgtggc ccggctggcc aaggagggtc tggagggggg gtatccctgt 1860
 gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc 1920
 attgatggcc gcggcgaggg cgggcatcat catcatcatc attaa 1965

<210> 12
 <211> 654
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 PL-deltaTaq

<400> 12
 Met Ile Thr Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg
 1 5 10 15
 Lys Lys Lys Lys Gly Gly Gly Val Thr Ser Gly Ala Thr Val Lys
 20 25 30
 Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
 35 40 45
 Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
 50 55 60
 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
 65 70 75 80

Glu	Leu	Leu	Gln	Met	Leu	Glu	Lys	Gln	Lys	Lys	Gly	Gly	Gly	Val	Thr	85	90	95
Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	100	105	110
Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	Leu	115	120	125
Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	Glu	130	135	140
Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	Ala	145	150	155
Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	Pro	165	170	175
Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	180	185	190
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	195	200	205
Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	Trp	210	215	220
Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val	225	230	235
Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	245	250	255
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	260	265	270
Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	275	280	285
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	290	295	300
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	305	310	315
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	325	330	335
Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	340	345	350
Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	355	360	365
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	370	375	380
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	385	390	395
Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	405	410	415
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	420	425	430
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	435	440	445
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	450	455	460
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	465	470	475
Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	485	490	495
Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	500	505	510
Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	515	520	525
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	530	535	540
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	545	550	555
																		560

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L18015F

<400> 17

tgacggagga taacgccagc ag

22

<210> 18

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L29930R

<400> 18

ggggttggag gtcaatgggt tc

22

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L30350F

<400> 19

cctgctctgc cgcttcacgc

20

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L35121R

<400> 20

cacatggtag agcaagcctg gc

22

<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L2089F

<400> 21

cccgtatctg ctgggatact ggc

23

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L7112R

<400> 22
cagcgggtgct gactgaatca tgg

23

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L30350F

<400> 23
cctgcctgcc gcttcacgc

19

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer L40547R

<400> 24
ccaatacccg tttcatcgcg gc

22

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer
H-Amelo-Y

<400> 25
ccacctcatc ctgggcacc

19

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial
Sequence:primerH-Amelo-YR

<400> 26
gcttgaggcc aaccatcaga gc

22

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
beta-globin primer Bglbn536F

<400> 27
ggttgccaa tctactccca gg 22

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
beta-globin primer Bglbn536R

<400> 28
gctcactcag tgtggcaaag 20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
beta-globin primer Bglbn1408R

<400> 29
gattagcaaa agggcctagc ttgg 24

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
tag

<400> 30
His His His His His His
1 5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
epitope tag

<400> 31
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 32
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 32
Gly Gly Val Thr
1

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 33
Gly Thr Gly Gly Gly Gly
1 5

<210> 34
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:lysine-rich
peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
1 5 10 15
Gly Gly Gly Val Thr
20